
Sequence Listing was accepted.

If you need help call the Patent Electronic Business Center at (866)

217-9197 (toll free).

Reviewer: Anne Corrigan

Timestamp: [year=2008; month=1; day=10; hr=15; min=58; sec=18; ms=788;]

Validated By CRFValidator v 1.0.3

Application No: 10593357 Version No: 2.0

Input Set:

Output Set:

Started: 2007-12-26 16:37:55.352

Finished: 2007-12-26 16:37:58.446

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 94 ms

Total Warnings: 86

Total Errors: 0

No. of SeqIDs Defined: 86

Actual SeqID Count: 86

Error code		Error Descript	ion								
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(1)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(2)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(3)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(4)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(5)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(6)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(7)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(8)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(9)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(10)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(11)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(12)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(13)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(14)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(15)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(16)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(17)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(18)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(19)
W	213	Artificial	or	Unknown	found	in	<213>	in	SEQ	ID	(20)

Input Set:

Output Set:

Started: 2007-12-26 16:37:55.352

Finished: 2007-12-26 16:37:58.446

Elapsed: 0 hr(s) 0 min(s) 3 sec(s) 94 ms

Total Warnings: 86

Total Errors: 0

No. of SeqIDs Defined: 86

Actual SeqID Count: 86

Error code Error Description

This error has occured more than 20 times, will not be displayed

SEQUENCE LISTING

<110>	BRAIN BIOTECHNOLOGY RESEARCH AND INFORMATION NETWORK AG Verseck, Stefan Liebeton, Klaus	
	Eck, Jurgen	
<120>	Nitrile hydratases from metagenome libraries	
<130>	009848-0356700	
<140>	10593357	
<141>	2007-12-26	
	WO PCT/EP2005/002556	
<151>	2005-03-10	
<150>	DE 10 2004 013 842.7	
	2004-03-20	
<160>	86	
<170>	PatentIn version 3.1	
<210>		
<211>		
<212>		
<213>	Artificial Sequence	
	Primer	
<400>	1	
gcsmrs	gcst gg	12
-		
<210>	2	
<211>	11	
<212>	DNA	
<213>	Artificial Sequence	
<220>		
<223>	Primer	
<400>	2	
ggscts	ccsc c	11
<210>	3	
<211>	11	
<212>		
<213>	Artificial Sequence	
<220>		
<223>	Primer	

<400> 3

11 ggsggsagsc c <210> 4 <211> 11 <212> DNA <213> Artificial Sequence <220> <223> Primer <220> <221> misc_feature <222> (3)..(3) <223> a or g or c or t/u<400> 4 ggncgcwbsg g 11 <210> 5 <211> 12 <212> DNA <213> Artificial Sequence <220> <223> Primer <220> <221> misc_feature <222> (3)..(3) <223> a or c <220> <221> misc_feature <222> (9)..(9) <223> a or g or c or t/u <400> 5 gcnmrrgcnt gg 12 <210> 6 <211> 11 <212> DNA <213> Artificial Sequence <220> <223> Primer

<220>

<221> misc_feature

<222> (3)..(3)

```
\langle 223 \rangle a or g or c or t/u
<220>
<221> misc_feature
<222> (6)..(6)
<223> a or g or c or t/u
<220>
<221> misc_feature
<222> (9)..(9)
\langle 223 \rangle a or g or c or t/u
<400> 6
ggnytnccnc c
                                                                          11
<210> 7
<211> 11
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (3)..(3)
\langle 223 \rangle a or g or c or t/u
<220>
<221> misc_feature
<222> (6)..(6)
\langle 223 \rangle a or g or c or t/u
<220>
<221> misc_feature
<222> (9)..(9)
<223> a or g or c or t/u
<400> 7
ggnggnarnc c
                                                                          11
<210> 8
<211> 11
<212> DNA
<213> Artificial Sequence
<220>
```

<223> Primer

```
<220>
<221> misc_feature
<222> (3)..(3)
\langle 223 \rangle a or g or c or t/u
<400> 8
gwngwrtccc a
                                                                       11
<210> 9
<211> 11
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u
<220>
<221> misc_feature
<222> (9)..(9)
<223> a or g or c or t/u
<400> 9
gcntggryng a
                                                                       11
<210> 10
<211> 11
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u
<220>
<221> misc_feature
<222> (9)..(9)
\langle 223 \rangle a or g or c or t/u
<400> 10
```

ggnytscene e

11

```
<210> 11
<211> 11
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u
<220>
<221> misc_feature
<222> (9)..(9)
<223> a or g or c or t/u
<400> 11
ggnggsarnc c
                                                                   11
<210> 12
<211> 11
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (3)..(3)
<223> a or g or c or t/u
<400> 12
                                                                   11
swnswrtccc a
<210> 13
<211> 12
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 13
gccaaggtcg tc
                                                                   12
<210> 14
```

<211> 11

```
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 14
ggccggtcct g
                                                                   11
<210> 15
<211> 15
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 15
tccttgtacc aggtc
                                                                   15
<210> 16
<211> 7
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 16
                                                                    7
gcccgcc
<210> 17
<211> 15
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 17
                                                                   15
ggcgctaaag ttgtt
<210> 18
<211> 12
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 18
tggccggttc tg
                                                                   12
```

```
<210> 19
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 19
caaattcttt ataccaagtc
                                                                   20
<210> 20
<211> 20
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 20
ccatatatcg catttcagct
                                                                   20
<210> 21
<211> 13
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 21
ggtcgtggcc aag
                                                                   13
<210> 22
<211> 11
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 22
                                                                   11
ggccggtcct g
<210> 23
<211> 15
<212> DNA
<213> Artificial Sequence
<220>
```

<223> Primer

```
tccttgtacc aggtc
                                                                   15
<210> 24
<211> 13
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 24
gcgcatttcg gcg
                                                                   13
<210> 25
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 25
gccaaggtcg tcgcsmrsgc stgg
                                                                   24
<210> 26
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 26
                                                                   22
ggccggtcct gggsctsccs cc
<210> 27
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<400> 27
                                                                   26
tccttgtacc aggtcggsgg sagscc
<210> 28
<211> 18
<212> DNA
<213> Artificial Sequence
```

<400> 23

```
<220>
<223> Primer
<220>
<221> misc_feature
<222> (10)..(10)
<223> a or c or g or t/u
<400> 28
gcccgccggn cgcwbsgg
                                                                       18
<210> 29
<211> 27
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (18)..(18)
<223> a or c or g or t/u
<220>
<221> misc_feature
<222> (24)..(24)
\langle 223 \rangle a or c or g or t/u
<400> 29
                                                                       27
ggcgctaaag ttgttgcnmr rgcntgg
<210> 30
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (15)..(15)
\langle 223 \rangle a or c or g or t/u
<220>
<221> misc_feature
<222> (18)..(18)
<223> a or c or g or t/u
```

```
<221> misc_feature
<222> (21)..(21)
<223> a or c or g or t/u
<400> 30
tggccggttc tgggnytncc nc
                                                                    22
<210> 31
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (23)..(23)
<223> a or c or g or t/u
<220>
<221> misc_feature
<222> (26)..(26)
<223> a or c or g or t/u
<220>
<221> misc_feature
<222> (29)..(29)
<223> a or c or g or t/u
<400> 31
caaattcttt ataccaagtc ggnggnarnc c
                                                                    31
<210> 32
<211> 31
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (23)..(23)
<223> a or c or g or t/u
<400> 32
                                                                    31
```

ccatatatcg catttcagct gwngwrtccc a

<220>

```
<210> 33
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (16)..(16)
<223> a or c or g or t/u
<220>
<221> misc_feature
<222> (22)..(22)
<223> a or c or g or t/u
<400> 33
                                                                     24
ggtcgtggcc aaggcntggr ynga
<210> 34
<211> 22
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (14)..(14)
\langle 223 \rangle a or c or g or t/u
<220>
<221> misc_feature
<222> (20)..(20)
<223> a or c or g or t/u
<400> 34
ggccggtcct gggnytsccn cc
                                                                     22
<210> 35
<211> 26
<212> DNA
<213> Artificial Sequence
<220>
```

<223> Primer

```
<220>
<221> misc_feature
<222> (18)..(18)
\langle 223 \rangle a or c or g or t/u
<220>
<221> misc_feature
<222> (24)..(24)
<223> a or c or g or t/u
<400> 35
tccttgtacc aggtcggngg sarncc
                                                                      26
<210> 36
<211> 24
<212> DNA
<213> Artificial Sequence
<220>
<223> Primer
<220>
<221> misc_feature
<222> (16)..(16)
<223> a or c or g or t/u
<400> 36
gcgcatttcg gcgswnswrt ccca
                                                                      24
<210>
      37
<211>
      705
<212> DNA
<213> Unknown
<220>
<223> Metagenome - alpha unit nitrile hydratase - M6aH6
<220>
<221> CDS
<222>
      (1)..(705)
<400> 37
                                                                      48
atg agc aag cac gta cac gat tac tac gcg aag aag aag cac gac cac
Met Ser Lys His Val His Asp Tyr Tyr Ala Lys Lys His Asp His
                5
                                    10
                                                        15
1
gat cat gac cac gac gtc cac gag gcg atc gag gac cgg gac gag ggt
                                                                       96
Asp His Asp His Asp Val His Glu Ala Ile Glu Asp Arg Asp Glu Gly
            20
                                25
                                                    30
```

ccg ccg Pro Pro				_		_	_	_		144
gaa gag Glu Glu 50										192
aag ttc Lys Phe 65										240
gcc tgg Ala Trp										288
gcc gcc Ala Ala		r Glu								336
gcg gtc Ala Val										384
tgc tcg Cys Ser 130	Cys Ty									432
aag agc Lys Ser 145										480
ctg aag Leu Lys										528
cac gac His Asp		n Ala								576
cag gga Gln Gly										624
cgc gac Arg Asp 210										672
cga aag Arg Lys 225			_			tag				705

<210> 38 <211> 234 <212> PRT <213> Unknown <220>
<223> Metagenome - alpha unit nitrile hydratase - M6aH6

<400> 38

Met Ser Lys His Val His Asp Tyr Tyr Ala Lys Lys His Asp His 1 5 10 15

Asp His Asp His Asp Val His Glu Ala Ile Glu Asp Arg Asp Glu Gly 20 25 30

Pro Pro Ser Glu Phe Glu Ile Met Ser Arg Ala Met Gln Glu Leu Leu 35 40 45

Glu Glu Lys Gly Val Val Thr Ala Glu Gln Val Arg Arg Ser Met Glu 50 60

Lys Phe Glu Glu Glu Leu Pro Tyr Arg Gly Ala Arg Val Val Ala His 65 70 75 80

Ala Trp Thr Asp Pro Glu Phe Lys Lys Arg Leu Leu Ala Asp Gly Lys
85 90 95

Ala Ala Val Ser Glu Phe Gly Ile Asp Leu Glu Ala Glu Arg Leu Ile 100 105 110

Ala Val Ala Asn Thr Thr Asp Val His Asn Val Ile Val Cys Thr Leu
115 120 125

Cys Ser Cys Tyr Pro Arg Thr Leu Leu Gly Met Pro Pro Thr Trp Tyr 130 135

Leu Lys Glu Phe Gly Thr Val Leu Pro Glu Arg Val Thr Val Arg Val

165
170
175

His Asp Ser Asn Ala Asp Met Arg Tyr Val Val Ile Pro Met Arg Pro
180 185 190

Gln Gly Thr Glu Gly Trp Ser Glu Glu Arg Leu Ala Glu Leu Leu Thr
195 200 205

Arg Asp Thr Leu Val Gly Val Thr Val Pro Lys Val Glu Val Gly Ser 210 215 220

Arg Lys Ser Lys Gly Gly Ser Lys Thr Arg 225 230												
<210> 39 <211> 657 <212> DNA <213> Unknown												
<220> <223> Metagenome - alpha unit nitrile hydratase - M12K24												
<220> <221> CDS <222> (1)(657)												
<400> 39												
atg tcg gac gga aca aca att gga atc cag gcc gcg aca acc ctt cga Met Ser Asp Gly Thr Thr Ile Gly Ile Gln Ala Ala Thr Thr Leu Arg 1 5 10 15	48											
tca gcc atg aac att cca gct cgt gaa ttc gcc ctc cag cgc act gcg Ser Ala Met Asn Ile Pro Ala Arg Glu Phe Ala Leu Gln Arg Thr Ala 20 25 30	96											
ccg gtc gag cag cgt gtc gac gcg atc cag gcg gcg ctc gac gaa cgc Pro Val Glu Gln Arg Val Asp Ala Ile Gln Ala Ala Leu Asp Glu Arg 35 40 45	144											
ggt ttg aac gcc agt gac gca gtc cag gaa ttg agc cac ctg gcg gag Gly Leu Asn Ala Ser Asp Ala Val Gln Glu Leu Ser His Leu Ala Glu 50 55 60	192											
gag caa tgg att ccg cgc aat ggc gcg cgg gtc gtc gcc aaa gcc tgg Glu Gln Trp Ile Pro Arg Asn Gly Ala Arg Val Val Ala Lys Ala Trp 65 70 75 80	240											
gtc gac ccg gaa ttc cgc gcg cgg ctt ctg gcc gac ggt cgc gcc gcc Val Asp Pro Glu Phe Arg Ala Arg Leu Leu Ala Asp Gly Arg Ala Ala 85 90 95	288											
gtt gcc gaa ctg ggc ctc tcg atg ccg aag cat cac cgg cac ctc gtg Val Ala Glu Leu Gly Leu Ser Met Pro Lys His His Arg His Leu Val 100 105 110	336											
gtg ctg gag aac acg ccg agc gtg cag aac gtc atc tgc tgc acg cag Val Leu Glu Asn Thr Pro Ser Val Gln Asn Val Ile Cys Cys Thr Gln 115 120 125	384											
	4											

tgc tcg tgc acg gcg ttc acg atc atc gga ctg ccg ccc gac tgg tac 432

Cys	Ser	Cys	Thr	Ala	Phe	Thr	Ile	Ile	Gly	Leu	Pro	Pro	Asp	Trp	Tyr	
	130					135					140					
aag	gac	ctg	gaa	tac	cgc	gcg	cga	gtc	gtc	cgg	gag	tcg	cgc	acc	gtg	480
Lys	Asp	Leu	Glu	Tyr	Arg	Ala	Arg	Val	Val	Arg	Glu	Ser	Arg	Thr	Val	
145					150					155					160	
ctg	aag	gag	atg	gga	ctg	gat	ctg	cct	cgg	gat	gtc	gaa	att	cgc	gtc	528
Leu	Lys	Glu	Met	Gly	Leu	Asp	Leu	Pro	Arg	Asp	Val	Glu	Ile	Arg	Val	
				165					170					175		
tgg	gat	acc	act	gcc	gac	acg	cgc	tac	atg	gta	ttg	ccg	gta	cag	ccg	576
Trp	Asp	Thr	Thr	Ala	Asp	Thr	Arg	Tyr	Met	Val	Leu	Pro	Val	Gln	Pro	